

BEST AVAILABLE COPY

RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH

#153
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6/15/01

JUN 12 2001

1600/2900

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/272,835A
Source: 1647
Date Processed by STIC: 5/24/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

09/272,835A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. Please **ensure your subsequent submission is saved in ASCII text**.

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
 In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

- 11 Use of <220> Sequence(s) 25 (and more) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

1647

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/272,835A

DATE: 05/24/2001

TIME: 17:52:27

Input Set : A:\PTO.txt

Output Set: C:\CRF3\05242001\I272835A.raw

5 <110> APPLICANT: Robert D. Klein
 6 Arnon Rosenthal
 7 Heidi S. Phillips
 8 Frederic J. de Sauvage
 10 <120> TITLE OF INVENTION: GFRalpha3 and its Uses
 12 <130> FILE REFERENCE: GENENT.065A
 14 <140> CURRENT APPLICATION NUMBER: US 09/272,835A
 15 <141> CURRENT FILING DATE: 1999-03-19
 17 <150> PRIOR APPLICATION NUMBER: US 60/079,124
 18 <151> PRIOR FILING DATE: 1998-03-23
 20 <150> PRIOR APPLICATION NUMBER: US 60/081,569
 21 <151> PRIOR FILING DATE: 1998-04-13
 23 <160> NUMBER OF SEQ ID NOS: 25

**Does Not Comply
Corrected Diskette Needed**

ERRORED SEQUENCES

1572 <210> SEQ ID NO: 25
 1573 <211> LENGTH: 17
 1574 <212> TYPE: DNA
 C--> 1576 <213> ORGANISM: Artificial
 W--> 1578 <220> FEATURE:
 W--> 1578 <223> OTHER INFORMATION:
 1578 <400> SEQUENCE: 25
 1579 acccagtcct ccctacc 17
 W--> 1582 W:\DOCS\BGY\SEQUENCE LISTING\GENENT.065A\GENENT.065ArevisedwithSubs.doc
 W--> 1583 042501
 E--> 1584 1
 E--> 1587 1

*This error appears throughout
Sequence Listing. Please check
all sequences*

*see item 11 on Error
summary sheet*

delete at end of file

PSI

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

DATE: 05/24/2001

PATENT APPLICATION: US/09/272,835A

TIME: 17:52:28

Input Set : A:\PTO.txt

Output Set: C:\CRF3\05242001\I272835A.raw

L:644 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:652 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:654 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:658 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:667 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L:669 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:669 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:675 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
L:677 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:677 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:683 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
L:685 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:685 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:1022 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18
L:1024 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1024 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:1355 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20
L:1357 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1357 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:1551 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:22
L:1553 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1553 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:1559 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:23
L:1561 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1561 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:1567 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:24
L:1569 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1569 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:1576 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:25
L:1578 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1578 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:1582 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:1583 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:1584 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:17 SEQ:25
L:1587 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:17 SEQ:25